

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:12:55 ; Search time 101.54 Seconds
(without alignments)
208.190 Million cell updates/sec

Title: Perfect score:
Sequence: US-09-052-089A-3
1 RTINKLFFDLAQEEENVLDRREFLNKLDNVRAQLSOKDKEKRDSQVYIDDLRDTLEERN 60
Database : BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5
Searched: 283138 seqs, 9089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match Length	DB ID	Description	Query Match Best Local Similarity	Score	DB ID
1	530	49.7	433	T3807	TRAF interacting protein - Fugu rubripes	530	T3807
2	170.5	16.0	1957	T3807	C-Species: Fugu rubripes	170.5	T3807
3	164.5	15.4	2116	A26555	C-Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000	164.5	A26555
4	163.5	15.3	1744	JH0220	C-Accession: T3007	163.5	JH0220
5	161	15.1	1325	T42722	R-Cottage, A. J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, FEBs Lett., 443, 370-374, 1999	161	T42722
6	160.5	15.1	1938	A40597	A-Title: Three receptor genes for plasminogen related growth factors in the genome of male enhanced anti	160.5	A40597
7	160.5	15.1	2017	T38071	A-Reference number: 220880; MUID:99148833	160.5	T38071
8	159.5	15.0	2139	T18296	A-Accession: T30807	159.5	T18296
9	159	14.9	1790	S67593	A-Status: preliminary; translated from GB/EMBL/DDBJ	159	S67593
10	158.5	14.9	1935	S06006	A-Molecule type: DNA	158.5	S06006
11	156.5	14.7	959	A5913	A-Residues: 1-433 <COT>	156.5	A5913
12	156.5	14.7	1138	T24635	A-Cross-references: EMBL:AJ010317; NID:el1355235; PID:el1355237; PIDN:CAA09084.1	156.5	T24635
13	155.5	14.6	1017	PC4035	A;Genetics:	155.5	PC4035
14	155.5	14.6	1164	T24806	A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	155.5	T24806
15	155.5	14.6	1203	B55094	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	155.5	B55094
16	155	14.5	1938	A5913	A;Cross-references: EMBL:AJ010317; NID:el1355235; PID:el1355237; PIDN:CAA09084.1	155	A5913
17	155	14.5	1940	A24922	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	155	A24922
18	154.5	14.5	1509	A27224	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	154.5	A27224
19	154	14.5	1177	B75150	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	154	B75150
20	153.5	14.4	1133	T22976	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	153.5	T22976
21	152.5	14.3	579	JH0820	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152.5	JH0820
22	152.5	14.3	1935	A37102	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152.5	A37102
23	152.5	14.3	1999	S21801	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152.5	S21801
24	152	14.3	1175	C35815	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152	C35815
25	152	14.3	1175	D35815	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152	D35815
26	152	14.3	1201	A35815	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152	A35815
27	152	14.3	1201	B35815	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152	B35815
28	152	14.3	2385	A32491	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	152	A32491
29	14.3	2411	2	B32491	A;Protein-protein interactions: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 380/3	14.3	B32491

RESULT 2

T3807

hypothetical coiled-coil protein - fission yeast (schizosaccharomyces pombe)

C-Species: Schizosaccharomyces pombe

C-Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C-Accession: T38077

R-Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, April 1996

A-Reference number: 221767

A-Status: preliminary; translated from GB/EMBL/DDJB

hypothetical protein - Streptomyces

myosin heavy chain

chromosome assembly

myosin heavy chain

364K Golgi complex

myosin heavy chain

plasminogen-bindin

hypothetical protein

conserved hypothetical protein

hypothetical protein

kinesin heavy chain

conserved hypothetical protein

kinesin heavy chain

A;Molecule type: DNA
 A;Residues: 1-1957 <CON>
 A;Cross references: EMBL:270690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06C
 A;Experimental source: strain 972n-; cosmid c1F3
 C;Genetics:
 A;Gene: SPDB:SPAC1F3.06C
 A;Map position: 1

Query Match	Best Local Similarity	Score	Length
QY 15 EENVLDRFLKNEIDNVRLAQQLSKQKEKRDQSIVITLDLTLEERNATVLSQOALGKAE	16 0%	170 5;	DB 2;
Db 1386 EDNQLATWNKLNQDHLNQEIRLUKEVKESIISLESLSNRQKSSLLDAKNEE	23 6%	Pred. No. 0.048;	Indices 43;
QY 75 -MLCSTLKKOMKYLEQQQDPTEKQAOEEAAGRRLRSRKMKT-----EQJELL-LOSOQP	53	Mismatches 58;	Gaps 6;
Db 1446 HMLDDTSRKNSLMEKIESINSSLDKSFEASAVEKLGAOKLHSSESLSLMENIKSQLQ	1445		
QY 124 EVEEMIRDQMGVGQGSAVEQELAVYCUSLKKYEN-----LKEARK	1445		
Db 1506 EAEKIQ---VDESTIQLDHEITASKNNYEGKLNDKDSIIRDLSENTEIHLNLLAEERS	161		
QY 162 ASGEVADKURKDLFSSRSKL-----QVYSELDQAKIELSKQDKDQSAKTEMSLRK	1562		
Db 1563 AVKLSTERKESELQFNNSRLADLEYHKSYQSELEGRSKKLAESTEEQLAENERLSLT	214		
QY 215 KLMILQ 220	1622		
Db 1623 RMLDLQ 1628	1622		

RESULT 3

A26655 myosin heavy chain [similarity] - slime mold (*Dictyostelium discoideum*)
 NC_Species: myosin ATPase (EC 3.6.1.32)
 C.Species: Dictyostelium discoideum
 C.Date: 05-Oct-1998 #sequence_revision 05-oct-1998 #text_change 02-Feb-2001
 C.Accession: A26655; S00250
 R.Warrick, H.M.; De Lozanne, A.; Levinand, L.A.; Spudich, J.A.
 Proc. Natl. Acad. Sci. U.S.A., 83, 9433-9437, 1986
 A;Title: Conserved protein domains in a myosin heavy chain gene from *Dictyostelium discoideum*
 A;Reference number: A26655; MUID:87092266
 A;Accession: A24728
 A;Molecule type: DNA
 A;Residues: 1-216 <WAR>
 A;Cross references: GB:MI14628; GB:MI1938; NID:9167834; PIDN:AAA33227.1; PID:91678
 R;DeLozanne, A.; Lewis, M.; Spudich, J.A.; Levinand, L.A.
 Proc. Natl. Acad. Sci. U.S.A., 82, 6807-6810, 1985
 A;Reference number: A24728; MUID:86016788
 A;Accession: A24728
 A;Molecule type: mRNA
 A;Residues: 2035-2116
 R;Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
 FEBS Lett. 227, 71-75, 1988
 A;Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium discoideum myosin heavy chain gene
 A;Reference number: S00250; MUID:88112226
 A;Accession: S00250
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 C;Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats.
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; F1-818-Domain; globular head <HEAD>
 F:89-747-/Domain: myosin motor domain homology <MMOT>
 F:179-186-/Region: nucleotide-binding motif A (P-loop)
 F:1819-2116-/domain: alpha-helical rod <ROD>

A;Accession: T42722
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: i-1325 <R0N>
 A;Cross-references: EMBL:D8270; NID:31096175; PID:81020389; PIDN:BAA19612.1
 C;Function: A;Experimental source: strain CD-1
 C;Description: supposed to play some role for spermatogenesis
 C;Keywords: leucine zipper

Query Match 15.1%; Score 161; DB 2; Length 1325;
 Best Local Similarity 23.1%; Pred. No. 0.11; Indels 52; Gaps 7;
 Matches 57; Conservative 48; Mismatches 90; Del 52; Insert 7;

Qy 13 QEEVNVLDFEFLKNELD----NVRQLSQKDKKEKRDQSVITDILRTDLERFNTAVSL 66
 Db 956 REINSILATEALARREADEVQLNQVQAVLQKREEDRQMLQVQALQSKRFKMEENSL 1025
 Qy 67 QOALGKA-----EMLCSTLKQMKYLEQQ---QDET 94
 Db 1026 KERQMAAARIEAGINRHHKAATILESEVKELQAKHLYVQTLQAEVDELQIQQDGKHSOI 1085

Qy 95 KOQEEAAGRRLRSKNTMPOIELLQILOSOLPVEVMIRDQVGGSSAVEQAVCVSLKEYE 154
 Db 1086 AQQTTELABARTOLQ----LIQKLQ--DEQMSQOPTGSQEMEDLKWELDOKERIO 1135

Qy 155 NUKEARKASGEVADKLRLDFSSRSKLSQLOTVYSLQDQAKLEKSKQDKLQSADKEIMSKK 214
 Db 1136 SLQDQDTEQDQ---KIELEGQQTQQTQTKISLEMVOEDLSPTQDKFEMLAKVSELN 1192

Qy 215 KL-TMLQ 220
 Db 1193 NMKFLLQ 1199

RESULT 6

A40997 myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians) #sequence_revision 31-dec-1993 #text_change 19-Jan-2001

C;Species: Aequipecten irradians
 C;Accession: A40997; S3557
 R;NIVTRAY, L.; GOODWIN, E.B.; Szent-Gyoergyi, A.G.
 A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Seq
 A;Reference number: A40997; MUID:92011595
 A;Accession: A40997
 A;Molecule type: mRNA
 A;Cross-references: GB:X5574; NID:95611; PIDN:CAA39247.1; PID:95612
 C;Superfamily: myosin heavy chain; myosin motor domain homology <NOT>
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide h
 F;176-183/Region: nucleotide-binding motif A (P-loop)
 F;547-586/Region: actin binding #status predicted
 F;53-675/Region: actin binding #status predicted <COI>
 F;836-1938/Region: S2
 F;1277-1938/Region: light meromyosin
 F;82/Binding site: ATP (Lys) #status predicted
 F;653,703/Active site: Cys #status predicted

Query Match 15.1%; Score 160.5; DB 2; Length 2168;
 Best Local Similarity 22.7%; Pred. No. 0.19; Indels 53; Gaps 7;
 Matches 58; Conservative 54; Mismatches 90; Del 53; Insert 7;

Qy 1 RTIINKLPLFDLAEFFENLIDREFLKNELDNYIAQLSKDKKEKRDQSVITDILRTLFERN 60
 Db 1592 QTWVEKL----KKQVSDLKRINKQQLDSENTELSQRNSQNKEE-----LKTLMQRL 1637

Qy 61 ATVVLSQLQALG----KEMLCSTLKQMKYLEQQDETQKQAE-EAGRLRSKMKTMEQI 114
 Db 1638 AEMICQREPGACTSEKQEQQENASLHYDWTQTSVLLSSAEISRKIOTHMEQ 1697

Qy 115 ELLIQSOLPEVEEMIR--DMVGQOSAVEQAVCVSLKEYENLKEARKASG----- 164
 Db 1698 NLLIKDELERLKLHRCPFLDSLQDQKMSVSVLSYNEKLLKEKEVLSEEELSKCADKLASSL 1757

Qy 165 -----EVADKLKDLSRSKIQTVYSELDAKLEKSKQDKLQ---- 203
 Db 1758 LEHRIATMKQEQTAWEEOQESLSKSQLAVSVQAVDLEDVQNLVOMAETIESDLQVTRQ 1817

Qy 204 --SADKEIMSLKKL 216
 Db 1818 KEAVKQEVNMSLRQL 1832

RESULT 8

T18296 myosin heavy chain - Entamoeba histolytica
 C;Species: Entamoeba histolytica
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
 C;Accession: T18296
 R;Guillen, N.
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2139 <GUT>
 A;Cross-references: EMBL:L03534; NID:91850912; PID:91850913; PIDN:AAB48065.1
 C;Genetics:
 A;Gene: mhcA
 C;Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 15.1%; Score 160.5; DB 1; Length 1938;
 Best Local Similarity 28.1%; Pred. No. 0.17; Indels 27; Gaps 7;
 Matches 55; Conservative 46; Mismatches 70; Del 27; Insert 7;

Qy 10 DLQAEENVLDREFLKNEL-DNVR--AQLSQDKKEKRDQSVITDILRTLERFNTAVVS 65
 Db 1055 DLKSTQENVEDLERYKRELEENNRKEABEISSLNSKLEDNVLVSOLRQIKLQLARIEE 1114

Qy 66 LQQLGKAEMLCSTLKKQMKYEQQQDETQKOAEEAGRRLRSKMTMEQIELLQSQPEV 125

F;91-780/domain: myosin motor domain homology <MMO>

Query Match 15.0%; Score 159.5; DB 2; Length 2139;
Best Local Similarity 24.0%; Pred. No. 0.21; No. 0.21;
Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

QY 5 NKLFFDL-AQEENNLDREFLKNFLDNVRAQLSOKERKRDQSVI-----ID 50
||: || : || : || | : || | : || | : || | : || | : || |
Db 1144 NKIEDLNRNQKIREKIDDBITKG - DV-SQYLOQKKEYSQIAKMQEERKIGNDKV 1200
||: || : || : || : || | : || | : || | : || | : || |
QY 51 TLDTLEERNATVWISLQALGKAEMCLSTLKKOMYLEDQODDETRQAOSEAGRRSKMT 110
|:||: |:||: |:||: |:||: |:||: |:||: |:||: |:||: |:||:
Db 1201 NKEKTIKEKELEIPIOSLQEKIDTEVEKEDAEKKREIEK--EMKALQEEKEVENESSKNS 1257
||: || : || : || : || | : || | : || | : || | : || |
QY 111 MEQIILLQSQLPVEEMIRDGMVGQSAVEQLAVCVSLKKEYENLKEARKASEVADL 170
||: || : || : || : || | : || | : || | : || | : || |
Db 1258 TEKDKEKLENDKLDQKLUDDMADNEKAKAKDQLEADLNEVDNHEKAVADELLNK 1317
||: || : || : || | : || | : || | : || | : || |
QY 171 R---KDLFSSRKLO-----TWYSELDAKLELSRKDLSA 205
||: || : || | : || | : || | : || | : || |
Db 1318 KAOSKELNLSLKAELTALELTAKASVYESKNDSNEKAELSETDQANEKLNQADLRKA 1377
||: || : || | : || | : || | : || |
QY 206 DKEIMSLKK 215
||: || : || | : || | : || |
Db 1378 TADLQEANEK 1387
||: || : || | : || |

RESULT 9
S67593 transport protein US01 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: Protein D2552; protein YDL058w
C;Species: *Saccharomyces cerevisiae*
C;Accession: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C;Accession: S67593; A38455; S30782
R;Bloecker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67597
A;Accession: S67593
A;Molecule type: DNA
A;Residues: 1-1790 <BLO>
A;Experimental source: strain S288C
R;Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonemura, T.; Yoda, K.; Yamasaki, M.
J. Cell Biol. 113, 245-260, 1991
A;Title: A cytoskeleton related gene, US01, is required for intracellular protein transp
A;Accession: A38455
A;Molecule type: DNA
A;Residues: 1-389 'A' 392-724, 'S' 726-1790 <NAK>
A;Cross-references: GB:X54378; PID:94777; PID:94778
A;Note: the authors translated the codon ACT for residue 768 as Ile
R;Hossettler, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.
submitted to the EMBL Data Library, February 1993
A;Description: An integrin analogue in *Saccharomyces cerevisiae*.
A;Reference number: S30782
A;Accession: S30782
A;Molecule type: DNA
A;Residues: 71-846 'E' 848-923 'K' 925-1252 'I' 1254-1318 'V' 1320-1460 'S' 1462-1580 'S'
A;Cross-references: EMBL:L03188
C;Genetics:
A;Gene: SGD:U501; INT1
A;Cross references: SGD:S0002216; MIPS:YDL058w
A;Map position: 4L
C;Keywords: coiled coil; transmembrane protein
F;326-342/Domain: transmembrane #status predicted <TM1>
F;344-410/Domain: transmembrane #status predicted <TM2>
F;617-633/Domain: transmembrane #status predicted <TM3>

Query Match 14.9%; Score 159; DB 2; Length 1790;
Best Local Similarity 23.7%; Pred. No. 0.19; No. 0.19;
Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

QY 1 RTINNLKFLDLAQ--EELNVLDREFLK-----NELDNTRAQLSOKERKRDQSVI 48
||: || : || : || | : || | : || | : || | : || | : || |
Db 1369 RKLLNEGSGSTTQYESEKINTLDELIRI-QNENELKAKEIDNTSEL-EKVLSND-- 1423
||: || : || | : || | : || | : || | : || | : || |
QY 49 IDTDLTLEERNATVWISLQ 7;
Db 1424 -----ELLEBKONTIKSLODEILSYDKITRNDEKLLSIERDKRDLESKQELRANQES 1478
||: || : || | : || | : || | : || | : || | : || |
QY 101 AGRLRSKMTMEQIETLLOSQLPVEEMIRDGMVGQSAVE---QLAVCVSLKKEVN 156
||: || : || | : || | : || | : || | : || | : || |
Db 1479 KAKYEGGLKLEESSEKAELEKSKEKEMKKL--ESTESNETELKSMETTRKSDEKL 1535
||: || : || | : || | : || | : || | : || | : || |
QY 157 KEARKASGEVADKLR-----KDLFSSRKLOTVV--SELDQAKLELKSA 199
||: || : || | : || | : || | : || | : || | : || |
Db 1535 EQSKSAEDPKIQHEKSDLISRINESKDIELKSKRIEAKSGSELETVKELNNQ 1595
||: || : || | : || | : || | : || | : || |
QY 200 KDQSADKEMSLKKL 216
||: || : || | : || | : || | : || |
Db 1596 EKIRINAEPENTVLKSKL 1612
||: || : || | : || | : || | : || |

RESULT 10
S60606 myosin beta heavy chain, cardiac muscle [similarity] - rat
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-dec-1993 #text_change 19-Jan-2001
C;Accession: S60606; S01536; I6741; AQ2989
R;Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
Nucleic Acids Res. 17, 7529-7530, 1989
A;Title: Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin
A;Reference number: S60606; MUID:90016823
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1935 <KRA>
A;Cross-references: EMBL:X15939; PID:956656; PID:CAA34065..1; PID:956657
R;McNamee, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.
J. Mol. Biol. 210, 665-671, 1989
A;Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison
A;Reference number: S07535; MUID:9013919
A;Accession: S07535
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-950 'R' 953-1935 <MCN>
R;Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.
Eur. Heart J. 5, 181-191, 1984
A;Title: Cardiac myosin heavy chain isozymic transitions during development and under
A;Reference number: I5305; MUID:85179510
A;Accession: I67441
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1871-1335 <RES>
A;Cross-references: GB:M32698; PID:g205598; PID:AAA41659..1; PID:g205599
R;Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
Nature 297, 659-660, 1982
A;Title: Molecular characterization of two myosin heavy chain genes expressed in the
A;Reference number: A02988; MUID:82220036
A;Accession: A02988
A;Molecule type: mRNA
A;Residues: 1524-1528 'V' 1530, 'R' 1532-1730, 'H' 1732-1783, 'K' 1785-1850, 'N' 1852-185
A;Cross-references: GB:J00727; PID:9205577; PID:AAA1654..1; PID:g205578
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F;88-766/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
F;58-588/Region: actin binding #status predicted
F;655-677/Region: actin binding #status predicted
F;839-195/Region: coiled coil #status predicted
F;839-1279/Region: light meromyosin
F;129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

F;184/Binding site: ATP (Lys) #status predicted
F;695,705/Active site: Cys #status predicted

Db 900 TDSKKEQDDLLVLLADQDQKILSLKSKL 927

RESULT 11						
A; Introns: 16/1; 124/3; 146/3; 204/1; 311/3; 358/3; 615/3; 900/2; 961/3; 1008/2; 1110						
rancytosis-associated protein p115 - rat ;Species: Rattus norvegicus (Norway rat)						
;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999						
Accession: A55913	Query	RTIINKLFLDIAQEBEENVLREF-LKNELENVRAVL-----SOKDEKR	Match	14.7%	Score	156.5;
Baroso, M.; Nelson, D.S.; Sztul, E.	Best Local Similarity	24.7%	DB	2;	Length	1138;
iroc. Natl. Acad. Sci. U.S.A. 92, 527-531, 1995	Local Conservative	45;	Pred. No.	0.16;	Mismatches	73;
Text: Transcytosis-associated protein (TAP)/p115 is a general fusion factor required	Matches	58;	Indels	59;	Gaps	9;
;Reference number: A55913; MUID:05132633	Db	544 KTIVENVY-LSEKQHLLSEINIKNEDMAVKRNSHQVAGLINEKSEEKKRKKQ	Qy	1	Qy	44
;Accession: A55913	Db	DSQVLTDLRDTLEERNATVLSLQQALGKAELM-CSTLKKQMKYLEQQDETQKOAQEEA	Qy	101	Db	603
;Status: preliminary	Db	DADV----TRLDEQONKL--LRQADSALLEEVQKGKREIDHLRQLAHQSEASGV	Qy	654	Db	102
;Molecule type: mRNA	Db	GRLRSKMKTMQIEELLIQLQSPLPEVEREMIRDGMVGQSAVEQPLAVCVSLKEYENIKEARK	Qy	161	Db	
;Residues: 1-959 <BAR>	Db		Qy		Db	
Cross-references: GB:U15589; NID:G558474; PIDN: AAC52151.1; PID:G558475	Db		Qy		Db	
Keywords: membrane fusion; membrane trafficking	Db		Qy		Db	

QY 178 RSKLOT---VYSELDOQAKLELKSQAOKDLSQASAKDEIMSLKKLTMLO 220
 A24222 I:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 myosin heavy chain, skeletal muscle, embryonic - rat
 N;Contains: myosin ATPase (EC 3.6.1.32)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C;Accession: A24922; A22538; B24263
 R;Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal-Ginard, B.
 J. Mol. Biol. 190, 291-317, 1986
 A;Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy
 A;Reference number: A24922; MUID:87060988
 A;Accession: A24922
 A;Molecule type: DNA
 A;Residues: 1-1940 <STR>
 A;Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:g1619328
 R;Strehler, E.E.; Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 468-471, 1985
 A;Title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes
 A;Reference number: A22538; MUID:85080119
 A;Accession: A22538
 A;Molecule type: DNA
 A;Residues: 1-168 <ST2>
 A;Cross-references: GB:B00370; GB:M10135; NID:9205580; PIDN:AA41655.1; PID:g554476
 R;Periasamy, M.; Wydro, R.M.; Strehler, E.E.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 15865-15862, 1985
 A;Title: Characterization of cDNA and genomic sequences corresponding to an embryonic myo-
 A;Reference number: A24263; MUID:86059474
 A;Accession: B24263
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:K03468; NID:g205573; PIDN:AAA41652.1; PID:g205574
 A;Experimental source: clone PMHC-72
 C;Genetics: 68/3; 116/3; 169/1
 A;Introns: 69/3; 119/3; 181/2
 A;Note: the list of intron positions may be incomplete
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo-
 F;92-775/Domain: myosin motor domain homology
 F;182-189/Region: nucleotide-binding motif A (P-loop)
 F;544-576/Region: actin binding #status predicted
 F;660-682/Region: actin binding #status predicted
 F;848-1277/Domain: coiled coil #status predicted <COI>
 F;1228-1247/Domain: hinge <HIN>
 F;1483-1509/Domain: carboxyl-terminal <CBT>
 F;133-Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted <CO2>
 F;188/Binding site: ATP (Lys) #status predicted
 Query Match 14 5%; Score 154 5%; DB 1; Length 1509;
 Best Local Similarity 25 8%; Pred. No. 0.28; Indels 55; Gaps 7;
 Matches 69; Conservative 52; Mismatches 91; Gaps 55; Gaps 7;
 QY 5 NKLFDLQQEENVLDRFLNEQNLNRQLSQRD-----KEKRSQ 46
 Db 894 DKLERDLAALKLKLDEKAQDADNLALLQKVAGLEELQETSSANDILEQKR 953
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co-
 F;89-767/Domain: myosin motor domain homology <MMOT>
 F;179-186/Region: nucleotide-binding motif A (P-loop)
 F;549-565/Region: actin binding #status predicted
 F;656-678/Region: actin binding #status predicted
 F;840-1940/Domain: coiled coil #status predicted <COI>
 F;1280/Region: S2
 F;1281-1290/Region: light meromyosin
 F;130-Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F;185/Birding site: ATP (Lys) #status Predicted
 F;196,706/Active site: Cys #status predicted
 Query Match 14 5%; Score 155; DB 1; Length 1940;
 Best Local Similarity 23 8%; Pred. No. 0.34; Indels 36; Gaps 7;
 Matches 53; Conservative 51; Mismatches 83; Gaps 36; Gaps 7;
 QY 24 LKNEIDLNVRAQLSKDKERDSQVILDTDRLERNATVVSQALGKRAEMCSTIKQ 83
 Db 1204 LAEQIDLNQVRVKQLEKEKESEKFLEKIDDDSSVE-----SVRSKANLEKICRTLEDO 1256
 QY 84 MKYLEQQQETQKA-----QEEAGRLLSKMKMTEQIELI---QSQIPEVEEM 128
 Db 1257 LSEARGKNEETQRSLSELTTQKSLQTEAGELSRQOLEKEESTVOLSRSKQAFQIEEL 1316
 QY 129 IRDMVGVGOSAVEQAVY-----CVSLKKEYENIKEARKASGEVADKURKDFFSRSKL 181
 Db 1317 KRLQEENENAKNALAHALQSSRHSODLURFQSESEQEGKAELQRALSKANSEWAQWRTK 1376
 QY 182 QT----VYSBLDQARLKLSAQKDLQSQADKEIMSLKKLTMLO 220
 Db 1377 ETDAQTQTELEAKKLL--AQR-LQDSEBQEAVNAKCASTLE 1416
 RESULT 18
 A27224 myosin heavy chain II - Acanthamoeba castellanii
 N;Contains: myosin ATPase (EC 3.6.1.32)
 C;Species: Acanthamoeba castellanii
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C;Accession: A27224
 R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
 J. Cell Biol. 105, 913-925, 1987
 A;Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle
 A;Reference number: A27224; MUID:87308395
 A;Accession: A27224
 A;Molecule type: DNA
 A;Residues: 1-1509 <HAM>
 A;Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAA68
 C;Genetics:
 A;Introns: 69/3; 119/3; 181/2
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo-
 F;182-189/Region: nucleotide-binding motif A (P-loop)
 F;544-576/Region: actin binding #status predicted
 F;660-682/Region: actin binding #status predicted
 F;848-1277/Domain: coiled coil #status predicted <COI>
 F;1228-1247/Domain: hinge <HIN>
 F;1483-1509/Domain: carboxyl-terminal <CBT>
 F;133-Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F;188/Binding site: ATP (Lys) #status predicted
 Query Match 14 5%; Score 154 5%; DB 1; Length 1509;
 Best Local Similarity 25 8%; Pred. No. 0.28; Indels 55; Gaps 7;
 Matches 69; Conservative 52; Mismatches 91; Gaps 55; Gaps 7;
 QY 47 VLIQDLRDLTLEERNATVVSQALGKAE-----MLCSTUQKMYLEQODD 92
 Db 954 AEKGELKASLEEERNRKALQEATKVESERNEQLDKYEDEAADHSILKKEEDLSRELR 1013
 QY 93 ETKQAOEEGR---LRSINKTMQIELLQISOLPEY-FEMIRGMVGQSAROLAVYC 147
 Db 1014 ETKQALADENISETLRKLNTERGADYDNVNELDVTATKQLEKTVSLEELAQTRA 1073
 QY 148 SLKKEYENIKEARKASGEVADKURKDFFSRSKQAFQIEEL 203
 Db 1074 QLEEB----KSKGRASSIAKQGQOLEDARSEVSDLSKSKLSEAEEKSIATKQNDRIIDE 1129
 QY 204 -----SADKEIMSLKKLTMLO 220
 Db 1130 QLEDBRTVRAVDQKOKKALEAKTELE 1156
 RESULT 19
 B75150 chromosome segregation protein (sncl) PAB2109 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C;Accession: B75150
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
 A;Reference number: A75001
 A;Accession: B75150
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-117 <RAW>	Qy 13 QEEENYL-DREFLKILDEYRAQLSOKDKKKRDS-QVITDPLRDLEERNAVWS--- 65	Db 153 IELTEKLLESEKESETAKTELEAVSKLUDSESENKFSDMTEAMKTOLINCEKKQDEA 212
A;Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PID:CAR49281.1; PID:9545779	Qy 114 IELLUQSOLPEVERMIRDGMVGQ-----SAVEQOLAVYCVSILKEYENLKEARKASGE 165	Qy : : : : : : : : : : : : : : : :
A;Experimental source: strain Orsay	Db 213 VELLKK-KLEEVERMSDVVKOLLESTTSEMVKHABAELIVVKQ--LEERQS-- 265	Db : : : : : : : : : : : : : :
C;Genetics:	Qy 166 VA-----DKLRKDLSRSRKLQTVYSELQ-----AKLELSKSAQDKLQADAKIMS 211	Qy : : : : : : : : : : : : : :
A;Gene: PAB2109	Db 349 IARWGRKRKEALLNKK-KELEEBRNKLWVKLGEBIDRTFAVAREEFDNVVKLELENARKSLYE 407	Db : : : : : : : : : : : : : :
C;Superfamily: chromosome segregation protein SMC1	Qy 212 LKKKLMLQ 220	Qy : : : : : : : : : : : : : :
Query Match 14.4%; Score 154; DB 2; Length 117; Best Local Similarity 22.9%; Pred. No. 0.23; Matches 57; Conservative 61; Mismatches 87; Indels 44; Gaps 10;	Db 408 NEADIKRLE 416	Db 266 -TENLKKDAENERN-LKTALESDESSAISEITKOMAEAKKELEASEKESELREQMDRLQ 323
RESULT 20	RESULT 21	RESULT 21
T22976 hypothetical protein F59A2.6 - caenorhabditis elegans	JH0820 160K golgi antigen - human (fragment)	JH0820 160K golgi antigen - human (fragment)
C;Species: Caenorhabditis elegans	C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)
C;Accession: T22976; T23157	C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000	C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
R;Lightning, J.	R;Fritzler, M.J.; Hamel, J.C.; Ochs, R.L.; Chan, E.K.L.	R;Fritzler, M.J.; Hamel, J.C.; Ochs, R.L.; Chan, E.K.L.
submitted to the EMBL Data Library, June 1994	J;Exp. Med. 178:49-62, 1993	J;Exp. Med. 178:49-62, 1993
A;Reference number: 219645	A;Title: Molecular characterization of two human autoantigens: unique cDNAs encoding A;Experimental source: hepatic carcinoma AT CC HB8065 cell line	A;Title: Molecular characterization of two human autoantigens: unique cDNAs encoding A;Experimental source: hepatic carcinoma AT CC HB8065 cell line
A;Accession: T22976	A;Reference number: JH0820; MUID:93301617	A;Reference number: JH0820; MUID:93301617
A;Status: Preliminary; translated from GB/EMBL/DDJB	A;Molecule type: mRNA	A;Molecule type: mRNA
A;Molecule type: DNA	A;Keywords: leucine zipper	A;Keywords: leucine zipper
A;Residues: 1-113 <WIL>	F;67-73/Region: proline-rich	F;67-73/Region: proline-rich
A;Cross-references: EMBL:234801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6	F;322-337/Region: glutamic acid-rich	F;322-337/Region: glutamic acid-rich
A;Experimental source: clone F59A2	F;419-455/Region: leucine zipper motif	F;419-455/Region: leucine zipper motif
R;Burton, J.		
A;Submitted to the EMBL Data Library, October 1995		
A;Accession number: 219700		
A;Status: preliminary; translated from GB/EMBL/DDJB		
A;Molecule type: DNA		
A;Residues: 1-113 <WIZ>		
A;Cross-references: EMBL:266514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6		
A;Experimental source: clone K01A1		
C;Genetics:		
A;Gene: CESP:F59A2.6		
Query Match 14.4%; Score 153.5; DB 2; Length 113; Best Local Similarity 25.0%; Pred. No. 0.24; Matches 60; Conservative 62; Mismatches 77; Indels 41; Gaps 10;	Query Match 14.3%; Score 152.5; DB 2; Length 579; Best Local Similarity 25.0%; Pred. No. 0.13; Matches 55; Conservative 42; Mismatches 86; Indels 37; Gaps 6;	Query Match 14.3%; Score 152.5; DB 2; Length 579; Best Local Similarity 25.0%; Pred. No. 0.13; Matches 55; Conservative 42; Mismatches 86; Indels 37; Gaps 6;
A;Map Position: 3 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 11/Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 11/	Db 363 REHNSLTALAKRREADDLVNLQVOAVLQRKEBEDRDKHLYQALQSALEKEKEKVNIS 422	Db 363 REHNSLTALAKRREADDLVNLQVOAVLQRKEBEDRDKHLYQALQSALEKEKEKVNIS 422
Db 483 AQFOQAELAARAQQLQQLQQL-----DEQFLSKQPVGQNEMLKMEVDQKEREIOSLKQQLD 539	Qy 113 --QIEL-----LQSOLPQEVEMRDGMVGQSAVEQOLAVYCVSILKEYENLKEARK 161	Qy 113 --QIEL-----LQSOLPQEVEMRDGMVGQSAVEQOLAVYCVSILKEYENLKEARK 161
Db 540 LTBOOG--RKELEGQQLQVNQYKSELEMAQEDLSMTQKD 576	Qy 162 ASEBVADKURDLFSRSRKLQTYSELQAKLEIJKSAQKD 201	Qy 162 ASEBVADKURDLFSRSRKLQTYSELQAKLEIJKSAQKD 201
RESULT 22	RESULT 22	RESULT 22
A7102 myosin beta heavy chain, cardiac and skeletal muscle - human	Nr:Contains: myosin ATPase (EC 3.6.1.32)	Nr:Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A37102; S12733; A9424; B28908; A2788; I154254; S12458; S09331; R;Jaenickke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bachem, G.;Genomics 8, 194-206, 1990	C;Accession: A37102; S12733; A9424; B28908; A2788; I154254; S12458; S09331; R;Jaenickke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bachem, G.;Genomics 8, 194-206, 1990	C;Accession: A37102; S12733; A9424; B28908; A2788; I154254; S12458; S09331; R;Jaenickke, T.; Diederich, K.W.; Haas, W.; Schleich, J.; Lichter, P.; Pfordt, M.; Bachem, G.;Genomics 8, 194-206, 1990
A;Title: The complete sequence of the human beta-myosin heavy chain gene and a comparison with the mouse beta-myosin heavy chain gene	A;Title: The complete sequence of the human beta-myosin heavy chain gene and a comparison with the mouse beta-myosin heavy chain gene	A;Title: The complete sequence of the human beta-myosin heavy chain gene and a comparison with the mouse beta-myosin heavy chain gene
A;Reference number: A37102; MUID:91055634	A;Reference number: A37102; MUID:91055634	A;Reference number: A37102; MUID:91055634
A;Accession: A37102	A;Accession: A37102	A;Accession: A37102
A;Molecule type: DNA	A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-1935 <JAF>	A;Residues: 1-1935 <JAF>	A;Residues: 1-1935 <JAF>
A;Cross-references: GB:M57965; GB:M30603; NID:9179507; PIDN:AA51837.1; PID:9179508; R;Lieuw, C.C.; Sole, M.J.; Yamauchi-Taihara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; Nuclic Acids Res 18, 3647-3651, 1990	A;Cross-references: GB:M57965; GB:M30603; NID:9179507; PIDN:AA51837.1; PID:9179508; R;Lieuw, C.C.; Sole, M.J.; Yamauchi-Taihara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; Nuclic Acids Res 18, 3647-3651, 1990	A;Cross-references: GB:M57965; GB:M30603; NID:9179507; PIDN:AA51837.1; PID:9179508; R;Lieuw, C.C.; Sole, M.J.; Yamauchi-Taihara, K.; Kellam, B.; Anderson, D.H.; Lin, L.; Nuclic Acids Res 18, 3647-3651, 1990
A;Title: Complete sequence and organization of the human cardiac beta-myosin heavy ch	A;Title: Complete sequence and organization of the human cardiac beta-myosin heavy ch	A;Title: Complete sequence and organization of the human cardiac beta-myosin heavy ch
A;Reference number: S12733; MUID:90301496	A;Reference number: S12733; MUID:90301496	A;Reference number: S12733; MUID:90301496

A;accession: S12733
A; molecule type: DNA
A; residues: 1-106, 'E', 108-671, 'LYH', 675-857, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',
A; cross-references: EMBL:X52889; NID:929726; PID:CA370681; PID:929727
R; Imauchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
Proc Natl Acad Sci U.S.A. 86, 3504-3508, 1989
A; title: Characterization of human cardiac myosin heavy chain genes.
A; reference number: A94224; MUID:8926452
A; molecule type: DNA
A; residues: 1-87, 'Q', 89-106, 'E', 108-177, 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1935
R; Yamauchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
Proc Natl Acad Sci U.S.A. 86, 7416-7417, 1989
A; reference number: A95226
A; contents: annotations erratum
R; Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
J. Clin. Invest. 82, 524-531, 1988
A; title: Molecular cloning and characterization of human cardiac alpha- and beta-form my
human atrium.
A; note: the authors translated the codon AGC for residue 108 as Arg
R; Richter, P.; Umada, P.K.; Levin, J.E.; Vosberg, H.P.
A; title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
A; reference number: A24997; MUID:87030293
A; molecule type: DNA
A; residues: 682-721, 975-1112, 1854-1935 <LIC>
A; cross-references: GB:X04627
R; Saez, L.J.; Gianola, K.M.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinwand
Nucleic Acids Res. 15, 5443-5459, 1987
A; title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A; reference number: A95669; MUID:87260010
A; accession: A27858
A; molecule type: DNA
A; residues: 1854-1865, 'A', 1867-1935 <SAE>
A; cross-references: GB:X05631; GR:Y00362; NID:934643; PID:CAA29119_1; PID:934644
R; Biederich, K.W.; Eisele, I.; Ried, T.; Jaenische, T.; Lichter, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1989
A; title: Isolation and characterization of the complete human beta-myosin heavy chain ge
A; reference number: 154254; MUID:89154425
A; status: translated from GB/EMBL/DDJB
A; molecule type: DNA
A; residues: 653-720 <RRSS>
A; cross-references: GB:M27636; NID:9179511; PID:AAA79019_1; PID:9601916
R; Rober, E.; submitted to the EMBL Data Library, January 1989
A; reference number: S12458
A; accession: S12458
A; molecule type: mRNA
A; residues: '785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>
A; cross-references: EMBL:X51591; NID:929467; PID:CA35940_1; PID:929468
R; Rober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A; title: Identification of three developmentally controlled isoforms of human myosin hea
A; reference number: S09331; MUID:90235862
A; accession: S09331
A; molecule type: mRNA
A; residues: '785-830, 'X', 832-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X'
, 1502-1670, 'X', 1672-1702, 'DE', 1705-1740, 'X', 1742-1810, 'X', 1812-1935 <BOW>
A; cross-references: EMBL:X51591
R; Jandreski, M.A.; Liew, C.C.
Hum. Genet. 76, 47-53, 1987
A; title: Construction of a human ventricular cDNA library and characterization of a beta
A; reference number: S02229; MUID:87192738
A; accession: S02229
A; molecule type: mRNA
A; residues: 1393-1702, DR', 1705-1935 <JAN>

A; cross-references: EMBL:X06976; NID:934860; PID:CA30039_1; PID:9825694
R; Saez, L.; Leinwand, L.A.
Nucleic Acids Res. 14, 2951-2969, 1986
A; title: Characterization of diverse forms of myosin heavy chain expressed in adult h
A; reference number: A93616; MUID:86176778
A; accession: B23767
A; molecule type: mRNA
A; residues: 'LLGGELASG', 1311-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LO', 14
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C; genetics:
A; gene: GDB:MYH7
A; cross-references: GDB:120215; OMIM:160760
A; map position: 14q12-4q12
A; introns: 67/3; 115/3; 168/1; 217/2; 213/3; 244/3; 266/1; 299/1; 333/3; 380/1; 419/3
24/3; 1390/2; 1451/3; 1507/1; 1508/3; 155/3; 1719/3; 1761/3; 1853/3; 1885/3; 1930/3
C; superfamily: myosin heavy chain; myosin motor domain homology
C; keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F; 88-765/domain: myosin motor domain homology <MM00>
F; 178-855/region: nucleotide-binding motif A (P-loop)
F; 548-585/region: actin binding #status predicted
F; 655-677/region: actin binding #status predicted
F; 839-1935/domain: coiled coil #status predicted <COI>
F; 1280-1935/region: light meromyosin
F; 129/modified site: No, N6, N6-trimethyllysine (Lys) #status predicted
F; 184/Binding site: ATP (Lys) #status predicted
F; 695,705/Active site: Cys #status predicted

Query	Match	Best Local Similarity	Score	DB	Length
QY	1 RTIINKLFLDAQEEENVILDR-----EFLK-----	20.5%	152.5	1	1935
Db	1129 RAKVEKLRDSLSELEERSTLEAGGATSVQLEMNKRAFAQMRDLEAFATLQEAT 1188				
QY	26 -----NELDVNRAQLSOKKDKERDSQVITDTDLTBERNATVVSQQA 69				
Db	1189 AAALRKKHADSVAVLGEOIDNLORVKOLEKESEKFKELEDDVTSNMQ-----IIKA 1241				
QY	70 LGAAEMCSTLKKOMKVLEQQDQETKQAEAGRLSMKT-----MEIELLIQS 121				
Db	1242 KANLEKMCRTLDQEMHNRSKABETQRVSNDLTSQRALKTENGELSROLDKEALI-SQ 1300				
QY	122 LP-----EVEMIRDMGVQGSQAVEQLAVCVVSKKEVENKEARKASGEV 166				
Db	1301 LTGKGLTYTQOLEDKROLLEEVAKKALAHQASARCDLUREQEEETAKELQV 1360				
QY	167 ADKLRKDLFSSRSRKLQT---VYSELDOAKLELKAQDLSQADKETMSLKKLTMLQ 220				
Db	1361 LSKRANEVQWQRIKYETDIAQTELEEAKKKL-AQR-LQEREAEVANAKCSSLE 1415				

RESULT 23
S21801 myosin heavy chain, neuronal [similarity] - rat
N; alternate names: myosin II
N; species: Rattus norvegicus (Norway rat)
C; species: Rattus norvegicus (Norway rat)
C; date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C; accession: S21801; PN0013; S18134
R; sun, W.; chantier, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A; title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian br
A; reference number: S21801; MUID:9225856
A; accession: S21801
A; molecule type: mRNA
A; residues: 1-1999 <SUN>
A; cross-references: EMBL:X62659
R; sun, W.; chantier, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A; title: A unique cellular myosin II exhibiting differential expression in the cerebr

A; Reference number: PNU013; MUID:91151356
A; Accession: PNU013
A; Molecule type: mRNA
A; Residues: 1914-1998, 'I' <SU2>
A; Experimental source: brain
C; Superfamily: myosin heavy chain: myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide
F; 84-763;/domain: myosin motor domain homology <MMOT>
F; 171-181;/Region: nucleotide-binding motif A (P-loop)
F; 541-575;/Region: actin binding #status predicted
F; 655-675;/Region: actin binding #status predicted
F; 1916-1999;/Domain: coiled coil #status predicted
F; 1836-1275;/Region: S2
F; 1277-1999;/Region: light meromyosin
F; 125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F; 180;/Binding site: ATP (Lys) #status predicted
F; 693-703;/Active site: CYS #status predicted
F; 1916;/Binding site: phosphate (Ser) (covalent) #status predicted
F; 1943;/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.3%; Score 152.5; DB 1; Length 1999;
Best Local Similarity 20.7%; Pred. No. 0.49; Matches 54; Conservative 54; Mismatches 88; Indels 65; Gaps 6;

QY 11 LAQEENNVLDRREF-----LNELLDNVRQLSQDKERDSDQVITDLRDTL 56
Db 1088 LARVEEAAQKNAKKKIRELESQISELQEDLESBRASKAKOKRDGEELALKTEL 1147

QY 57 BERNATVVSQALGKAEMCSTLKQM-----KYLEQQDETOKA 97
Db 1148 EDLTDSSTAQELRSKREQEVENILKKTLEBAAKTHEAQIQEMROKHSQAVEELAEQLEQT 1207

QY 98 QEEAGRLSRKMT-----QIELLOS-----QIPEVEEMIRDMGV---GQSAV 139
Db 1208 RKRVKANLAKQTLNERNGLANEVNVKLQLOGDRSEHKRVEQLOELQVKNEGERRV 1267

QY 140 EQAVYCVSLLKKKEYENLKERKASGEVADKLRLDFSSRSKLTQVYSELQAKLELKSQ 199
Db 1268 TELABKVTKLQVELDNVTGULQSOSKSLTQFSALESQ 1313

QY 200 KDLGSAKETMSLKKLKLTMQ 220
Db 1314 ELQOBENRQKLSLSTKLQVE 1334

RESULT 25
D35815 D35815
Myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 13-Feb-1998
C;Accession: D35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-995, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion t
A;Reference number: A35815; MUID:90346288
A;Accession: D35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for resi
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain: myosin motor domain homology
C;Keywords: ATP

Query Match 14.3%; Score 152; DB 2; Length 1175;
Best Local Similarity 23.9%; Pred. No. 0.3; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;

C35815 C35815
myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: C35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Reference number: A35815; MUID:90346288
A;Accession: C35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155; NID:gb219; PIDN:CAA7308_1; PRD:92546935
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: Flybase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match 14.3%; Score 152; DB 2; Length 1175;
Best Local Similarity 23.9%; Pred. No. 0.3; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;

QY 11 LAQEENNVLDRREF-----LNELLDNVRQLSQDKERDSDQVITDLRDTL 57
Db 789 LEQEENKVLAQL--ELSQVREIDRR--QEKEREFENTRKNHORALDSMSQALEAEGK 845

QY 58 -----ERNATVVSQALGKAEMCSTLKQM-----KYLEQQDETOKA 98
Db 846 KAEALRMKKKLEADINELTALDHANKANAEQKNKIQYQQQDKIQPALEEQRARDDA 905

QY 109 KTMQIEL-----LLQSQLEPEMIRMGVGOSAVEOLAVCVSLLKKKEYENLKERKA 162
Db 906 R-EQLGISERRANALONEESRTLQEQADGRRQAEO----ELADAHEQNEVAQ 957

QY 163 SGEVADKLRLDFSSRSKLTQVYSELQAKLELKSQ 201
Db 958 NASISAARK---LESEQTLHSIDLDELLNEAKNSEERAKKAMVDAARLADELRAEDDH 1013

QY 202 LQSADKEIMSLKKLKLTMQ 220
Db 1014 AQTOEKLRALEQQIKEQ 1032

RESULT 26
A35815 A35815
myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster

C;date: 12-Oct-1990 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
 C;accession: A35815
 R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
 Genes Dev. 4, 885-895, 1990
 A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
 A;Reference number: A35815; MUID:90346288
 A;Accession: A35815
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1201 <COL>
 A;Cross-references: EMBL:X53155; NID:98219; PIDN:CAA37310_1; PID:92546938
 A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
 C;Genetics:
 A;Gene: FlyBase:Mhc
 A;Cross-references: FlyBase:FBgn0002741
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: AtP

Query Match 14.3%; Score 152; DB 2; Length 1201;
 Best Local Similarity 23.9%; Pred. No. 0.31; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 C;Species: Drosophila melanogaster
 Qy 11 LAQEEENVIDREFLKNEEDNVRAQLSQKDEKEK-----RDSQVILDTRDITLE---- 57
 Db 789 LEQEEENKVIRLAQL---ELSQVRQIDRRIQEKEEFENTRKHORALDSMQASLEAKG 845
 Qy 58 -----ERNATVVSLSQALGKAEMCSTLKKOMKYLEQODETKQAOEGRRSKM 108
 Db 846 KAELRMKKLEADINELFIALDHANKANAEQKNRYQQQLDQTALEEBORADD 905
 Db 906 R-EOLGISERRANALONEESRTLHQADGRQRROEQ-----ELADAHEOLNEYSAQ 957
 Qy 163 SGEVADKLRLDFSSRSKQTVSELDQ-----AKL--ELKSQKD 201
 Db 958 NASISAARK---LESLOQTLSHSDLDLINEAKNSEEKAKKAMDAARLADELRAEDH 1013
 Qy 202 LOSADKEIMSLKKLTMLQ 220
 Db 1014 AQTOEKLRALEQQIKELO 1032

RESULT 27
 B35815
 myosin heavy chain 2, muscle - fruit fly (*Drosophila melanogaster*) (fragment)
 C;Species: *Drosophila melanogaster*
 C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
 C;Accession: B35815
 R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
 Genes Dev. 4, 885-895, 1990
 A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
 A;Reference number: A35815; MUID:90346288
 A;Accession: B35815
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1201 <COL>
 A;Cross-references: EMBL:X53155; NID:98219; PIDN:CAA37311_1; PID:92546939
 A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
 C;Genetics:
 A;Gene: FlyBase:Mhc
 A;Cross-references: FlyBase:FBgn0002741
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: AtP

Query Match 14.3%; Score 152; DB 2; Length 2385;
 Best Local Similarity 23.9%; Pred. No. 0.63; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 C;Species: Drosophila melanogaster
 Qy 11 LAQEEENVIDREFLKNEEDNVRAQLSQKDEKEK-----RDSQVILDTRDITLE---- 57
 Db 1999 LEQEEENKVIRLAQL---ELSQVRQIDRRIQEKEEFENTRKHORALDSMQASLEAKG 2055
 Qy 58 -----ERNATVVSLSQALGKAEMCSTLKKOMKYLEQODETKQAOEGRRSKM 108
 Db 2055 KAELRMKKLEADINELFIALDHANKANAEQKNRYQQQLDQTALEEBORADD 2115
 Db 2116 R-EOLGISERRANALONEESRTLHQADGRQRROEQ-----ELADAHEOLNEYSAQ 2167
 Qy 163 SGEVADKLRLDFSSRSKQTVSELDQ-----AKL--ELKSQKD 201
 Db 2168 NASISAARK---LESLOQTLSHSDLDLINEAKNSEEKAKKAMDAARLADELRAEDH 2223
 Qy 202 LOSADKEIMSLKKLTMLQ 220
 Db 2224 AQTOEKLRALEQQIKELO 2242

Query Match 14.3%; Score 152; DB 2; Length 1201;
 Best Local Similarity 23.9%; Pred. No. 0.31; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 C;Species: Drosophila melanogaster
 Qy 11 LAQEEENVIDREFLKNEEDNVRAQLSQKDEKEK-----RDSQVILDTRDITLE---- 57

RESULT 28
 A32491
 myosin heavy chain 1, muscle - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 12-Oct-1990 #sequence_revision 31-Dec-1993 #text_change 07-Feb-2001
 C;Accession: A32491
 R;George, E.L.; Ober, M.B.; Emerson Jr., C.P.
 Mol. Cell. Biol. 9, 2957-2974, 1989
 A;Title: Functional domains of the *Drosophila melanogaster* muscle myosin heavy-chain
 A;Reference number: A32491; MUID:89384556
 A;Accession: A32491
 A;Status: preliminary
 A;Molecule type: DNA; mRNA
 A;Residues: 1-2385 <GEO>
 A;Cross-references: GB:MG1229; GB:M27194
 A;Note: the authors translated the codon TGC for residue 329 as Ser
 C;Genetics:
 A;Gene: FlyBase:Mhc
 A;Cross-references: FlyBase:FBgn0002741
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: AtP; nucleotide binding; P-loop
 F;137-1032/Domain: myosin motor domain homology #status atypical <MMO>
 F;227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 14.3%; Score 152; DB 2; Length 2385;
 Best Local Similarity 23.9%; Pred. No. 0.63; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 C;Species: Drosophila melanogaster
 Qy 11 LAQEEENVIDREFLKNEEDNVRAQLSQKDEKEK-----RDSQVILDTRDITLE---- 57
 Db 1999 LEQEEENKVIRLAQL---ELSQVRQIDRRIQEKEEFENTRKHORALDSMQASLEAKG 2055
 Qy 58 -----ERNATVVSLSQALGKAEMCSTLKKOMKYLEQODETKQAOEGRRSKM 108
 Db 2055 KAELRMKKLEADINELFIALDHANKANAEQKNRYQQQLDQTALEEBORADD 2115
 Db 2116 R-EOLGISERRANALONEESRTLHQADGRQRROEQ-----ELADAHEOLNEYSAQ 2167
 Qy 163 SGEVADKLRLDFSSRSKQTVSELDQ-----AKL--ELKSQKD 201
 Db 2168 NASISAARK---LESLOQTLSHSDLDLINEAKNSEEKAKKAMDAARLADELRAEDH 2223
 Qy 202 LOSADKEIMSLKKLTMLQ 220
 Db 2224 AQTOEKLRALEQQIKELO 2242

RESULT 29
 B32491
 myosin heavy chain 2, muscle - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*

C;date: 12-Oct-1989 #sequence_revision 31-dec-1993 #text_change 02-Feb-2001
 C;Accession: B32491
 R;George, E.L.; Ober, M.B.; Emerson Jr., C.P.
 Mol. Cell. Biol. 9, 2957-2974, 1989
 A;Title: functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene
 A;Accession: B32491
 A;Status: preliminary
 A;Molecule type: DNA; mRNA
 A;Residues: 1-2411 <GEO>
 A;Cross-references: GB:M61229; GB:M27194
 C;Genetics:
 A;Gene: FlyBase:Mhc
 A;Cross-references: FlyBase:FBgn0002741
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: ATP; nucleotide binding; p-loop
 F;227-234/Region: nucleotide-binding motif A (P-loop)
 Query Match 14.3%; Score 152; DB 2; Length 2411;
 Best Local Similarity 23.9%; Pred. No. 0.63; Mismatches 84; Indels 64; Gaps 9;
 Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;
 QY 11 LAQEBENVLREFLKNELDNVRQLSQKKEK-----RDSQVIIIDLRTDLE---- 57
 Db 1999 LEQEBENKVLAQL---ELSQVRQIDRRIQEKFEPFENTRKHORALDSMQASLEAEKG 2055
 QY 58 -----ERNATVVSQOALGKAGEMLCSLTKKOMKYLEQQDETETKAQEEGRLRSM 1018
 Db 2056 KAEALRMKKKLEADINEIETALDHANKANAEAKNQNIKRYQQQLKDQTAYALEEFOARODA 2115
 QY 109 KTMQIEL-----LLQSLPEVEMIRMGVGQSVEAQOLAVYCISLKKEYENKEARKA 152
 Db 2116 R-SQLGTSERRANALQNLNEESRSRMLQDAGRGRQEQ-----ELADAHEPDNEVSQ 2167
 QY 163 SGEVADKLKDLSRSSLQTVVSELDQ-----AKL--ETKSAQKD 201
 Db 2168 NASISAALKR---LESELQTLSDLELLNEAKKANSEEAKKANVDAARLADLRAEQDH 2223
 QY 202 LQSADEKREIMSLKKLTMLQ 220
 Db 2224 AQTOEKLRLKALEQOIKELO 2242

RESULT 30
 T17272 hypothetical protein DKFZp44B0435.1 - human
 C;Species: Homo sapiens (man)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
 C;Accession: T17272; T46451; A36881
 R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A;Reference number: 218723
 A;Accession: T17272
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1780 <POU>
 A;Cross-references: EMBL:AL117496
 A;Experimental source: adult testis; clone DKFZp44B0435
 R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A;Accession: T46451
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 555-1136, 'C', 1138-1608, 'K', 1610-1780 <AAA>
 A;Cross-references: EMBL:AL17392
 A;Experimental source: adult testis; clone DKFZp4341152
 R;Westendorf, J.M.; Rao, P.N.; Gerace, L.
 Proc. Natl. Acad. Sci. U.S.A. 91, 714-718, 1994
 A;Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MPM2 monoclonal

A;Reference number: A36881; MUID:94119956
 A;Accession: A36881
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1215-1361, 'E', 1263-1418, 'S', 1420-1608, 'K', 1610-1780 <WES>
 A;Cross-references: GB:LJ782; MUID:929328; PID: AAC7542.1; PID: 9592329
 C;Genetics:
 A;Note: DKFZp434B0435.1; DKFZp4341152.1
 C;Keywords: phosphoprotein
 Query Match 14.2%; Score 151.5; DB 2; Length 1780;
 Best Local Similarity 21.3%; Pred. No. 0.49; Mismatches 50; Indels 39; Gaps 6;
 Matches 50; Conservative 62; Mismatches 84; Indels 39; Gaps 6;
 QY 22 EFLKNELDNVRQL-SQKD-----KEK-----RDSQVIIIDLRTDLEERNAT--- 62
 Db 1039 EELSQIEKLOQEVKGKQENNRLLKEKNODDLKKRKTLLQQLKEERQKLNQEVTLVQ 1098
 QY 63 ---WVSQOALGKAEMLCSTLKKOMYLEQQDETETKAQEEAGRURSKMKTMBQIELIQ 119
 Db 1099 IQRHVEGKRALSETQGYCYKAKIKEITLEYQKVERSNSAKLEQDILEKESILK 1158
 QY 120 SOLPVEEMLRDMGVGOSAVEQOLAVYCISLKKEYENL-----KARAKASGE 165
 Db 1159 RNLKEFOEHLQD--SVKNTKDLNVKEILKEETIOTLNQNDMKHLIQLKEEEETNRQ 1215
 QY 165 VADKURKDFFSRSKLQTYSELDQAKLELKSQADKELMSLKKLMLQ 220
 Db 1216 ETEKLUKEESSASSARTONIKADLQKEEYDADKEKLTDKOKIQVKOREVSMR 1270

RESULT 31
 S54871 M protein - Streptococcus sp.
 C;Species: Streptococcus sp.
 C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
 C;Accession: S54871
 R;Podbielski, A.; Melzer, B.
 submitted to the EMBL Data Library, June 1991
 A;Reference number: S54871
 A;Accession: S54871
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-532 <POD>
 A;Cross-references: EMBL:X60097; MUID:9840905; PID:CAA42693.1; PID:9840906
 C;Superfamily: M5 protein

Query Match 14.2%; Score 151; DB 2; Length 532;
 Best Local Similarity 23.0%; Pred. No. 0.15; Mismatches 62; Indels 52; Gaps 8;
 Matches 62; Conservative 52; Mismatches 93; Indels 62; Gaps 8;

Db 174 YDLFEELGKKLKENQDLEEKLKDFKEFYIGETLRVINSDELKLGQLNNDIDKHLRQE 233
 QY 38 KDKKRRDSQVITDYLRTDLEERNATVVSQOALGKAEMLCSTLKKOMYLEQQDETETKAQ 97
 Db 234 KQKAEADROT-L-ELEKAKLEEEKQIISDARSQSLRSRDLDSREAKKQLEYORLEEKQI 292
 QY 98 QEEAGR-LRSKMKTMEQIELLQSQLPVEE-----MIRDGVGOSAVEQOLAVY 145
 Db 293 SDASRQSLRHDLDASREAKKQLEYQKLEEQNKESEARSKGLRRLDASREAKKQED 352
 QY 145 CVSLSKKEYENLKEARKKASEGEVADKLKDFFSSRSKLTQVSELDQAKLELKSQ---KDL 202
 Db 353 LANLTAELDKVKEEKQISDASRKGLRRLDASREAKKQLEYORLEEKQI 412
 QY 203 OSAK-----EIMSLKKI 216
 Db 413 EESKRLTEKEAKLQAKLKEAKALKEKU 441

R; Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.
J. Biol. Chem. 270, 1395-1401, 1995
A; Title: A xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34
A; Reference number: A55441; MUID:95138137
A; Accession: A55441
A; Status: preliminary
A; Molecule type: protein
A; Residues: 198-232 <KEL>
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: nucleotide binding; P-loop
F; 88-787/Domain: myosin motor domain homology <MMOT>
F; 178-185/Region: nucleotide-binding motif A (P-loop)

Query Match_h 14.1%; Score 150.5; DB 2; Length 1992;
Best Local Similarity 22.9%; Pred. No. 0.63; Mismatches 85; Indels 53; Gaps 9;
Matches 58; Conservative 57; Mismatches 85; Indels 53; Gaps 9;

Db 1430 KEALKENKSLQEQBLSSARDAVEHLTKSLADVESQSVQNEKDALLGKLALQERDKL 1489
Oy 144 V-----YCVSISK----- 150
Db 1490 VEMDKSLENOSLGSCESEKSLAAGGLTEDKEKLMKELSVRSCKIAESTEWQEKHKELQ 1549
Qy 151 KEYENLKARKASGEVADKLRKFSSRKLQTYSELQAKLELSAQDKLQSADKEIM 210
Db 1550 KEYEVLLQSYENVSNEARIQHVVWESVRQEQVYAKLSSAESDKRERKQLQDAEOME 1609
Qy 211 SLKKKI 216
Db 1610 EMKEKM 1615

RESULT 36
JC5837
364K Golgi complex-associated protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Accession: JC5837
C; Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
R; Toki, C.; Fujiwara, T.; Sonda, M.; Hong, H.S.; Misumi, Y.; Ichihara, Y.
Cell Struct. Funct. 22, 565-577, 1997
Article: Identification and characterization of rat 364-kDa Golgi-associated protein rec
A; Reference number: JC5837; MUID:98093490
A; Accession: JC5837
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-3187 <TOK>
A; Cross-references: DDBJ:D25543; NID:9516825; PIDN:BA05026.1; PID:9516826
C; Comment: This protein plays a role in the formation and maintenance of the characteris
F; 49-549, 624-176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status predict
F; 3165-3187/Domain: membrane anchor #status predicted <MDA>

Query Match_h 14.1%; Score 150.5; DB 2; Length 3187;
Best Local Similarity 19.0%; Pred. No. 1; Mismatches 58; Conservative 59; Indels 99; Gaps 7;
Matches 58; Conservative 59; Mismatches 90; Indels 99; Gaps 7;

Db 1310 DLQAQEENNVIDREFLKN--ELDNVRAQLSKDKEKR-----DSQVITDLRTLEER 59
Oy 10 DLQAQEENNVIDREFLKN--ELDNVRAQLSKDKEKR-----DSQVITDLRTLEER 59
Db 1310 ELESSQLKTADLEHLKTLOPELETQKHYQKEEREVSYLVQGQGEKEQLTTVQTEMEO 1369
Qy 60 NATVVL-----QQLAGKAEMLCSTLKKOMKYLQQQ----- 91
Db 1370 ERLIKALHQTELEMQAKEHSERLKVQVECELEKKQPKELEEEAKQQLQRKQLQALISR 1429
Qy 92 -----DETQKQAEAGRRLRSM---KTMQIELLQSQSLPVEEMIRDGVGQSAVEOLAVCVSLKEYENLKEAR-- 160

RESULT 37
S39082 myosin heavy chain, embryonic - chicken (fragment)
C; Species: Gallus gallus (chicken)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999
C; Accession: S39082; S24349; A30170; S1265
R; Moore, L.A.; Arrizubietta, M.J.; Tidyanian, W.E.; Herman, L.A.; Bandman, E.
submitted to the EMBL Data Library, August 1991
A; Description: Analysis of the chicken fast myosin heavy chain family: Localization o
A; Reference number: S39081
A; Accession: S39082
A; Molecule type: mRNA
A; Residues: 1-741 <MOO>
A; Cross-references: EMBL:M74086
A; Experimental source: clone Cemb3
R; Moore, L.A.; Arrizubietta, M.J.; Tidyanian, W.E.; Herman, L.A.; Bandman, E.
A; Title: Analysis of the chicken fast myosin heavy chain family. Localization o
A; Reference number: S24348; MUID:92309413
A; Accession: S24349
A; Molecule type: mRNA
A; Residues: 1-12, 14-741 <MOO2>
A; Cross-references: EMBL:M74086
A; Experimental source: clone Cemb3
R; Labrutta, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
DNA 8, 39-50, 1989
A; Reference number: A30170; MUID:89210285
A; Accession: A30170
A; Molecule type: DNA
A; Residues: 723-741 <LAG>
A; Cross-references: GB:MA4691; NID:9341219; PIDN:AAA48950.1; PID:9531186
R; McCarthy, J.G.; Heywood, S.M.
Nucleic Acids Res. 15, 8069-8085, 1987
A; Title: A long poly(pyrimidine/polypurine tract induces an altered DNA conformation o
A; Reference number: S01265; MUID:88040428
A; Accession: S01265
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A; Cross-references: EMBL:X06251; NID:953600; PIDN:CAA29593.1; PID:963601
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; muscle

Query Match_h 14.1%; Score 150; DB 2; Length 741;
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